

the reference and target hybridization patterns without sequencing the target polynucleotide.

11. (Amended) The method of claim 1, wherein the microarrays are arranged in parallel.
12. (Twice amended) A method of determining whether two or more target polynucleotides are identical without sequencing the target polynucleotides, comprising the steps of:
  - (a) providing at least two identical polynucleotide probe microarrays, wherein each probe comprises a double stranded region and a single-stranded n-mer overhang region such that the overhangs in each microarray constitute a complete set of n-mers, wherein each n-mer is at least 8 nucleotides in length;
  - (b) hybridizing first target polynucleotide to said overhangs of probe polynucleotides in one microarray to generate a first hybridization pattern;
  - (c) hybridizing second target polynucleotide to said overhangs of probe polynucleotides in a second microarray to generate a second hybridization pattern; and
  - (d) comparing the first and second hybridization patterns.
18. (Amended) The method of claim 12, wherein the microarrays are arranged in parallel.

#### REMARKS

Applicant has carefully reviewed and considered the Office Action mailed on September 18, 2001, and the references cited therewith.

Claims 1-18 are pending in this application. Claims 1 and 12 are independent claims and have been amended to clarify the meaning of "n-mer" by inserting "wherein each n-mer is at least 8 nucleotides in length" and to clarify the meaning of "array" by substituting "microarray" therefor. The term "array" in dependent claims 11 and 18 has also been amended to "microarray." These amendments are made to clarify the claimed subject matter of the application.